# Efficient Segmentation Pipeline using Diffeomorphic Image Registration: A Validation Study

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Motivation: Functional measurements of the left atrium (LA) in atrial fibrillation (AF) patients is limited to a single CINE slice midway through the LA. Nonetheless, a full 3D characterization of atrial functional measurements would provide more insights into LA function. But this improved modeling capacity comes at a price of requiring LA segmentations of each 3D time point, a time-consuming and expensive task that requires anatomy-specific expertise. We propose an efficient pipeline which requires ground truth segmentation of a single (or limited) CINE time point to accurately propagate it throughout the sequence. This method significantly saves human effort and enable better characterization of LA anatomy. **Methods:** From a gated cardiac CINE MRI sequence we select a single CINE time point with ground truth segmentation, and assuming cyclic motion, we register other images corresponding to all time points using diffeomorphic registration in ANTs. The diffeomorphic registration fields allow us to map a given anatomical shape (segmentation) to each CINE time point, facilitating the construction of a 4D shape model. **Results:**
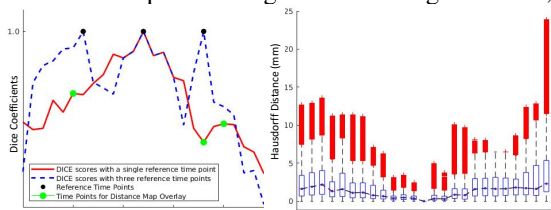
(Left): Represents the dice scores for a patient across all CINE time points with, *(Right):* Represents the per vertex Hausdorff distances in mm for a patient across all CINE time points *(only 9.577% are red marked outliers)*
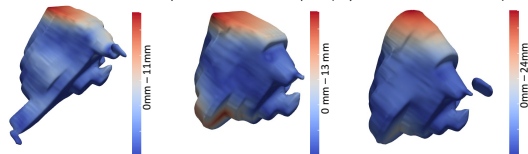
This figure represents the green time points highlighted in *top left plot.* Each figure has a distance map overlay which shows the deviation from the closest reference point.

We have a set of 5 CINE sequences with segmentation performed and reviewed by a clinical expert. With a single reference time point, we get Dice coefficients 0.83 ± 0.1 and Hausdorff distances 1.37 ± 0.86 mm. We achieve better DICE scores with 3 reference time points, which indicates better segmentation. **Conclusion:** The proposed method facilitates an efficient process of LA segmentation. With just segmenting a single or few time points, we can obtain accurate segmentation for the entire sequence, which can be used as is or as drivers for better algorithms.